



SEQUENCE LISTING

<110> MASUDA, ESTEBAN

<120> METHODS OF SCREENING CYCLIC PEPTIDES AND
IDENTIFYING TARGETS THEREFOR

<130> RIGL-023

<140> 10/533,144
<141> 2005-04-27<150> US03/27370
<151> 2003-08-30<150> 60/407,385
<151> 2002-08-30

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1227
<212> DNA
<213> Artificial Sequence<220>
<223> synthetic oligonucleotide<220>
<221> CDS
<222> (1)...(1227)<220>
<221> misc_feature
<222> 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171
<223> n = A,T,C or G<400> 1
atg gag agc ggc agc ccc gag atc gag aag ctg agt cag agc gac atc 48
Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
1 5 10 15tat tgg gac agc atg gtg agc atc acc gag acc ggc gtg gag gag gtg 96
Tyr Trp Asp Ser Met Val Ser Ile Thr Glu Thr Gly Val Glu Val
20 25 30ttc gac ctg acc gtg ccc ggc ccc cac aac ttc gtg gcc aac gac atc 144
Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
35 40 45atc gtc cac aac agc nnn nnn nnn tgc atc agc ggc gac agc ctg 192
Ile Val His Asn Ser Xaa Xaa Xaa Cys Ile Ser Gly Asp Ser Leu
50 55 60atc agc ctg gcc agc acc ggc aag agg gtg agc atc aag gac ctg ctg 240
Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu
65 70 75 80

gac gag aag gac ttc gag atc tgg gcc atc aac gag cag acc atg aag Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys 85 90 95	288
cta gag agc gcc aag gtg agc agg gtg ttc tgc acc ggc aag aag cta Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu 100 105 110	336
gtg tac atc cta aga acc agg cta ggc agg acc atc aag gcc acc gcc Val Tyr Ile Leu Arg Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala 115 120 125	384
aac cac agg ttc cta acc atc gac ggc tgg aag agg cta gac gag cta Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu 130 135 140	432
agc cta aag gag cac atc gcc cta ccc cg ^g aag cta gag agc agc Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser 145 150 155 160	480
cta cag cta ggc ctc cgc ggc cag atc gat gtg agc aag ggc gag gag Leu Gln Leu Gly Leu Arg Gly Gln Ile Asp Val Ser Lys Gly Glu Glu 165 170 175	528
ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val 180 185 190	576
aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr 195 200 205	624
tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 210 215 220	672
gtg ccc tgg ccc acc ctc gtg acc acc ctg acc cac ggc gtg cag tgc Val Pro Trp Pro Thr Leu Val Thr Leu Thr His Gly Val Gln Cys 225 230 235 240	720
ttc agc cgc tac ccc gac cac atg aag cag cac gac ttc ttc aag tcc Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser 245 250 255	768
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 260 265 270	816
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 275 280 285	864
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 290 295 300	912
aac atc ctg ggg cac aag ctt gag tac aac ttc aac agc cac aac gtg Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val 305 310 315 320	960

tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	325	330	335	1008
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys				
atc cgc cac aac atc gag gac gga tcc gtg cag ctc gcc gac cac tac	340	345	350	1056
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr				
cag cag aac acc cca att ggc gac ggg ccc gtg ctg ctg ccc gac aac	355	360	365	1104
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn				
cac tac ctg agc acc cag agc gct ctt tcg aaa gac ccc aac gag aag	370	375	380	1152
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys				
cgc gat cat atg gtc ctg ctc gag ttc gtg acc gcc gcc ggg atc act	385	390	395	1200
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr				
ctc ggc atg gac gag ctg tac aag taa	405			1227
Leu Gly Met Asp Glu Leu Tyr Lys *				

<210> 2
 <211> 408
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> VARIANT
 <222> 54, 55, 56, 57
 <223> Xaa = Any Amino Acid

<220>
 <223> synthetic oligonucleotide

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 Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
 1 5 10 15
 Tyr Trp Asp Ser Met Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
 20 25 30
 Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
 35 40 45
 Ile Val His Asn Ser Xaa Xaa Xaa Cys Ile Ser Gly Asp Ser Leu
 50 55 60
 Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu
 65 70 75 80
 Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys
 85 90 95
 Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Leu
 100 105 110
 Val Tyr Ile Leu Arg Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala
 115 120 125
 Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu
 130 135 140
 Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser
 145 150 155 160
 Leu Gln Leu Gly Leu Arg Gly Gln Ile Asp Val Ser Lys Gly Glu Glu
 165 170 175

Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val
180 185 190
Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr
195 200 205
Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
210 215 220
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr His Gly Val Gln Cys
225 230 235 240
Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser
245 250 255
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
260 265 270
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
275 280 285
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
290 295 300
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val
305 310 315 320
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
325 330 335
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
340 345 350
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
355 360 365
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
370 375 380
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
385 390 395 400
Leu Gly Met Asp Glu Leu Tyr Lys
405

<210> 3
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide

<400> 3
Gly Ser Gly Gly Ser
1 5

<210> 4
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide

<400> 4
Ala Gly Pro Ile
1